

## **Claims**

What is claimed is:

1. A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are symmetrically related and compete to effect gene expression regulation.
2. A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are symmetrically related and cooperate to effect gene expression regulation.
3. A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are asymmetrically related and compete to effect gene expression regulation.
4. A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are asymmetrically related and cooperate to effect gene expression regulation.
5. A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are symmetrically related and compete to effect gene expression regulation.
6. A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are symmetrically related and cooperate to effect gene expression regulation.

7. A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are asymmetrically related and compete to effect gene expression regulation.
8. A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are asymmetrically related and cooperate to effect gene expression regulation.
9. A method of genome investigation comprising identifying a new class of connectrons that bind to the major groove of double-stranded DNA in two directions.
10. A method of genome investigation comprising designing one or more new classes of connectrons that bind to the major groove of double-stranded DNA in two directions.
11. A method of genome investigation comprising identifying the relationship between an existing pair of connectrons in a genome.
12. A method of genome investigation comprising designing the relationship between a synthetic pair of connectrons in a genome.
13. A method for identifying the relationship between an existing pair of connectrons in a genome that act in a competitive mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes.
14. A method for designing a synthetic pair of connectrons in a genome that act in a competitive mode such that with respect

to the individual connectrons there is an increased lifetime of connectron control of a set of genes.

15. A method for identifying the relationship between an existing pair of connectrons in a genome that act in a cooperative mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes.

16. A method for designing a synthetic pair of connectrons in a genome that act in a cooperative mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes.